Figure 2 shows a nucleic acid sequence from a cDNA isolated from PoEV having the sequence of SEQ ID NO: 2.

Figure 3 shows a nucleic acid sequence from a cDNA isolated from PoEV having the sequence of SEQ ID NO: 3. Also depicted are the amino acid sequences produced by the 3 ORFs encoded by SEQ ID NO: 3 including (i) the *gag* gene encoding for a polypeptide having the amino acid sequence of SEQ ID NO: 4 (corresponding to nucleotides 588-2162 of SEQ ID NO: 3); (ii) the *pol* gene encoding for a polypeptide having the amino sequence of SEQ ID NO: 5 (corresponding to nucleotides 2163-5747 of SEQ ID NO: 3); and (iii) the *env* gene encoding for a polypeptide having the amino sequence of SEQ ID NO: 6 (corresponding to nucleotides 5620-7590 of SEQ ID NO: 3).

Figure 4 (top) shows a list of changes to the PoEV nucleic acid sequence (as compared to the sequence depicted in Figure 3) which were found in PoEV DNA isolated from PoEV infected Raji cells. The bottom half shows a list of changes to the ENV polypeptide (as compared to the sequence depicted in Figure 3) resulting from the nucleotide changes shown in the top half of the figure. SEQ ID NO: 9 is a nucleic acid sequence corresponding to nucleotides 5260-8210 of SEQ ID NO: 3 and containing the specified modifications. SEQ ID NO: 10 is an amino acid sequence corresponding to the ENV polypeptide of SEQ ID NO: 6 and containing the specified modifications.

Figure 5 shows a phylogenetic tree for the POL polypeptide.

Figure 6 the nucleotide sequence for a portion of the PoEV genome corresponding to the U3 region and depicting the multiple potential transcription sites located therein (SEQ ID NO: 17).

Detailed Description of the Invention

On page 23, please replace the second full paragraph with the following paragraph:

The changes at base nos. 5902 and 7700 do not effect the corresponding amino acid sequence. However, the changes at positions 2121 and 2157 alter the amino acid sequence at the end of GAG and the beginning of POL. For GAG the final amino acid "S" have now been

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replaced by "VLALEEDKD" (SEQ ID NO: 15). The total product size is now 524 amino acids. For POL, the first five amino acids "RLGET" (SEQ ID NO: 16) have been deleted and replaced by "GRR". The total product size is now 1194 amino acids.

On page 28, please replace the paragraph beginning at the top of the page with the following:

Oligonucleotides were selected from the PoEV genome.

The upstream primer was 5'-GGA AGT GGA CTT CAC TGA G-3' (SEQ ID NO: 7).

The downstream primer was 5'-CTT TCC ACC CCG AAT CGG-3' (SEQ ID NO: 8).

On page 29, please replace the second paragraph with the following:

Two further oligonucleotides were designed against the 3' end of the *pol* gene and 5' end of the *gag* gene respectively.

The 3' *pol* oligonucleotide was 5'-GAT GGC TCT CCT GCC CTT TG-3' (SEQ ID NO: 11).

The 5' *gag* oligonucleotide was 5'-CGA TGG AGG CGA AGC TTA AGG-3' (SEQ ID NO: 12).

On page 32, please replace the paragraph following the heading PCR with the following:

Oligonucleotides were selected from the PoEV genome.

The upstream primer was 5'-GAT GGC TCT CCT GCC CTT TG-3' (SEQ ID NO: 13)

5' base position: 5240.

The downstream primer was 5'-CCA CAG TCG TAC ACC ACG-3' (SEQ ID NO: 14)

5' base position: 8144.

Expected product size: 2904 bp.

On page 34, please replace the text following "Phylogenetic analysis" with the following:

Phylogenetic analysis was performed using the PHYLIP package. Sequence distances were calculated using the PROTDIST program (Dayhoff matrix) and a neighbour-joining unrooted phylogenetic tree reconstructed using the NEIGHBOUR program.

Bootstrapping was performed using 200 replicates of the *pol* alignment, created using the SEQBOOT program and a consensus tree was obtained using the CONSENSE program (see Figure 5). The bootstrap percentages are indicated at the branch fork, with missing values equal to 100%. The data indicate that PoEV is closely related to but distinct from the type-C oncovirus typified by gibbon, murine and feline leukaemia viruses.

A phylogenetic tree was constructed from the *pol* alignment using the maximum likliehood algorithm (Dayhoff matrix). This tree differed from the *pol* NJ tree only in the placement of the BaEV lineage in relation to other mammalian type C viruses and corresponded to a low bootstrap for the BaEV fork observed in the NJ tree.

IN THE CLAIMS:

Pursuant to 37 C.F.R. §1.121(c)(3), please cancel claims 1-43 and replace them with new claims 44-66 as set forth below. A marked-up version of the claims showing the changes made follows the remarks section of this response.

44. (New)   An isolated polynucleotide fragment comprising:

(a)   a nucleotide sequence set forth in SEQ ID NO: 1, 2, 3 or 9;

(b)   a portion of a nucleotide sequence set forth in (a) which encodes for at least one porcine retrovirus polypeptide;

(c)   a nucleotide sequence which has at least 75% identity to a sequence set forth in (a) or (b); or

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